WHAT IS CLAIMED IS:

1. A method for analyzing the sequence of a template comprising:

(a) capturing the template;

(b) scanning the captured template using a primer-polymerase complex for regions of complementarity to the primer;

(c) extending the primer by one or more nucleotide moieties by means of a template-homology dependent extension reaction; and

(d) detecting the extended primer,

wherein detection of the extended primer indicates the presence of one or more regions of complementarity to the primer in the captured template.

2. The method of Claim 1 wherein the primer comprises a polynucleotide of 3 to 7 bases.

3. A method for analyzing the sequence of a template nucleic acid according to the methods of Claim 1, wherein the steps of the method are repeated for an array of primer-polymerase complexes so that a pattern of signals is generated for the template.

4. The method of Claim 3 wherein the array is an array of sequence reagents, each sequence reagent comprising:

(i) a capture moiety;

(ii) a spacer moiety; and

(iii) a primer region.

5. The method of Claim 4 wherein the sequence reagents are immobilized to a solid surface.

6. The method of Claim 5 wherein the solid surface is glass or plastic.

435/6

Boyce-Jacino et al.
fd 6-16-98

7. The method of Claim 5 wherein the solid surface is a glass plate, a quartz wafer, a nylon membrane, a nitrocellulose membrane, or a silicon wafer.

8. The method of Claim 5 wherein the solid surface is silicon glass.

9. The method of Claim 5 wherein the solid surface is polystyrene plastic.

10. The method of Claim 4 wherein the sequence reagent further comprises an attachment moiety.

11. The method of Claim 10 wherein the attachment moiety is located at or near the 5'-terminus of the sequence reagent.

12. The method of Claim 10 wherein the attachment moiety is an amino group, a thiol group, a disulfide group, or a biotin group.

13. The method of Claim 4 wherein the capture moiety is on a first reagent and the primer region is on a second reagent.

14. The method of Claim 13 wherein the first reagent is proximal to the second reagent on a solid phase.

15. The method of Claim 4 wherein the capture moiety comprises a sequence of 8-24 cytosine bases.

16. The method of Claim 4 wherein the capture moiety comprises a specific sequence complementary to a PCR primer or a portion thereof.

17. The method of Claim 4 wherein the spacer region is at least 10 Å in length.

18. The method of Claim 4 wherein the spacer region comprises a random, pseudo-random, or non-random sequence of nucleotide bases or analogs thereto.

19. The method of Claim 1 wherein the nucleotide moieties are non-chain terminating nucleotides or nucleotide analogues.

20. The method of Claim 19 wherein the nucleotide moieties are deoxynucleoside triphosphate bases or ribonucleoside triphosphate bases.

21. The method of Claim 1 wherein the nucleotide moiety is a chain terminating nucleotide analogue.

22. The method of Claim 21 wherein the chain terminating nucleotide analogue is a dideoxynucleotide.

23. The method of Claim 1 wherein the nucleotide moiety is detectably labeled.

24. The method of Claim 23 wherein the detectable label is a fluorescent label.

25. The method of Claim 23 wherein the detectable label is a radioactive isotope.

26. The method of Claim 23 wherein the detectable label is an electron rich molecule.

27. The method of Claim 1 wherein the extended primer is detected by change in mass.

28. The method of Claim 4 wherein the density of sequence reagents in the array is at least 1000 elements/cm^2.

29. A sequence array comprising one or more sequence reagents in an orderly arrangement wherein each reagent comprises:

(i) a capture moiety which can form a stable complex with a region of a template nucleic acid molecule;

(ii) a spacer region; and

(iii) a primer region, wherein said primer region comprises 3-7 bases.

30. The sequence array of Claim 29 wherein the array comprises a set, subset, or combination of 4^3 - 4^7 different sequence reagents.

add B3

ADD L=6